AMENDMENTS TO THE SPECIFICATION

Please amend the Specification to read as follows:

Replace paragraph [0007] in the Specification of the above-identified application with the following paragraph:

[0007] Efforts are also underway to define so-called minimal bacterial genomes for growth under defined conditions and, similarly, to identify genes essential for growth under defined conditions. Determining the content required for a minimal bacterial genome is of intense interest. One approach is to assemble the theoretical minimal genome in silico by comparing a variety of different microbial genomes. Alternatively, the smallest genome amongst existing genomes (mycoplasma) can be analyzed by mutagenesis. E.coli K12 is a preferred bacterium, because of [[it]] its simplicity in handling, and its short generation time. It is desirable to try to generate a minimal or significantly reduced E. coli K12 genome, which may shorten the already short doubling time in rich media.

Replace paragraph [0022] in the Specification of the above-identified application with the following paragraph:

[0022] FIG. 1 depicts a pair of preferred arrangements of full-length and interleaved (compressed) transposase-binding sequences that face in opposite directions. The full-length version of the IE/OE linker (Linker A) is accorded SEQ ID NO: 1, and the corresponding compressed version of the IE/OE linker is accorded SEQ ID NO: 2. Likewise, the full-length version of the IE/ME linker (Linker B) is accorded SEQ ID NO: 3, and the corresponding compressed version of the IE/ME linker is accorded SEQ ID NO: 4.

Replace paragraph [0048] in the Specification of the above-identified application with the following paragraph:

[0048] In one approach, depicted in Fig. 2, a transposon that confers resistance to selectable marker ~~SMI~~ SM1 is transposed into a first gene using Tnp1 to produce an initial insert library. Using Tnp2, the products of that library are transposed into a second gene to form fusion proteins. More particularly, each of a pair of genes A and B is provided on a

separate construct that also comprises an origin of replication and distinct selectable markers, SM2 and SM3, respectively. Gene A contributes its N-terminal portion, and Gene B contributes its C-terminal portion, to the fusion protein. In this approach, the construct that contains Gene A also includes a single Tnp2 transposase-interacting sequence upstream of the gene's promoter.

Replace paragraph [0049] in the Specification of the above-identified application with the following paragraph:

[0049] The aforementioned Gene A construct is then mixed with a pre-cleaved transposon that includes yet another distinct selectable marker ~~(SM-1)~~ (SM1) flanked at a first end by a first Tnp1-specific transposase-interacting sequence, and at a second end by a transposase-interacting sequence pair having a Tnp2-specific sequence and a second Tnp1-specific sequence, where the Tnp2-specific sequence is between the selective marker and the second Tnp1-specific sequence. In a first transposition reaction between these two nucleic acid molecules in the presence of an amount of Tnp1 effective to catalyze transposition, the transposon inserts into the target construct at random positions, some of which are in Gene A. Reaction products are then transformed into suitable host cells, such as *E. coli* cells, under standard transformation conditions. Electroporation is a suitable transformation method. The transformed cells are grown under selective pressure (SM1 and SM2) for cells that contain constructs having the Gene A construct and an integrated transposon. The resulting selected cells constitute the initial library of random linker inserts.